

21437
Ser. No.
09/529, 043

SEQUENCE LISTING

<110> Forschungszentrum Juelich GmbH

<120> Method for microbial production of amino acids of the aspartate and/or glutamate family and agents which can be used in said method

<130> 1

<140> 09/529, 043

<141> 2000-04-03

<150> PCT/EP98/06210

<151> 1998-09-30

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 3728

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (165)..(3587)

<223> pyruvate carboxylase

<400> 1

cgcaaccgtg cttgaagtctg tgcaggtcag gggagtgttg cccgaaaaca ttgagaggaa 60

aacaaaaacc gatgtttgat tggggaaatc gggggttacg atactaggac gcagtgactg 120

aataattac tcta gtg tcg act cac 176

ctatcacccct tggcggtctc ttgttcaaag gaataattac tcta gtg tcg act cac

Val Ser Thr His

1

aca tct tca acg ctt cca gca ttc aaa aag atc ttg gta gca aac cgc 224
Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu Val Ala Asn Arg

5 10 15

20

ggc gaa atc gcg gtc cgt gct ttc cgt gca gca ctc gaa acc ggt gca 272
Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu Glu Thr Gly Ala

25 30 35

gcc acg gta gct att tac ccc cgt gaa gat cggt gga tca ttc cac cgc 320



Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly Ser Phe His Arg
 40 45 50
 tct ttt gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc 368
 Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val
 55 60 65
 aag gcg tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt 416
 Lys Ala Tyr Leu Asp Ile Asp Glu Ile Gly Ala Ala Lys Lys Val
 70 75 80
 aaa gca gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc 464
 Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala
 85 90 95 100
 cag ctt gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca 512
 Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro
 105 110 115
 acc cca gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc 560
 Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr
 120 125 130
 gcc gcg aag aag gct ctg cca gtt ttg gcg gaa tcc acc ccg agc 608
 Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser
 135 140 145
 aaa aac atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc 656
 Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro
 150 155 160
 atc ttt gtg aag gca gtt gcc ggt ggc gga cgc ggt atg cgt ttt 704
 Ile Phe Val Lys Ala Val Ala Gly Gly Arg Gly Met Arg Phe
 165 170 175 180
 gtt gct tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt 752
 Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg
 185 190 195
 gaa gct gaa qcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct 800
 Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala
 200 205 210
 gtg att aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act 848
 Val Ile Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr
 215 220 225
 gga gaa gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt 896

Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg
 230 235 240 944
 cac caa aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa
 His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu
 245 250 255 260 265 270 275 992
 ctg cgt gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att
 Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile
 280 285 290 1040
 ggt tac cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc
 Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly
 295 300 305 1088
 aac cac gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc
 Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr
 310 315 320 325 330 335 340 1136
 gtg act gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc
 Val Thr Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg
 345 350 355 1184
 ttg gct gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag
 Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys
 360 365 370 375 380 385 390 1232
 atc aag acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat
 Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp
 395 400 405 1280
 cca aac aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc
 Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg
 410 415 420 425 430 435 440 1328
 tca cca ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt
 Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly
 445 450 455 460 465 470 475 480 1376
 ggc gaa atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc
 Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys
 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995 1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200 1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560 1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620 1625 1630 1635 1640 1645 1650 1655 1660 1665 1670 1675 1680 1685 1690 1695 1700 1705 1710 1715 1720 1725 1730 1735 1740 1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860 1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980 1985 1990 1995 2000 2005 2010 2015 2020 2025 2030 2035 2040 2045 2050 2055 2060 2065 2070 2075 2080 2085 2090 2095 2100 2105 2110 2115 2120 2125 2130 2135 2140 2145 2150 2155 2160 2165 2170 2175 2180 2185 2190 2195 2200 2205 2210 2215 2220 2225 2230 2235 2240 2245 2250 2255 2260 2265 2270 2275 2280 2285 2290 2295 2300 2305 2310 2315 2320 2325 2330 2335 2340 2345 2350 2355 2360 2365 2370 2375 2380 2385 2390 2395 2400 2405 2410 2415 2420 2425 2430 2435 2440 2445 2450 2455 2460 2465 2470 2475 2480 2485 2490 2495 2500 2505 2510 2515 2520 2525 2530 2535 2540 2545 2550 2555 2560 2565 2570 2575 2580 2585 2590 2595 2600 2605 2610 2615 2620 2625 2630 2635 2640 2645 2650 2655 2660 2665 2670 2675 2680 2685 2690 2695 2700 2705 2710 2715 2720 2725 2730 2735 2740 2745 2750 2755 2760 2765 2770 2775 2780 2785 2790 2795 2800 2805 2810 2815 2820 2825 2830 2835 2840 2845 2850 2855 2860 2865 2870 2875 2880 2885 2890 2895 2900 2905 2910 2915 2920 2925 2930 2935 2940 2945 2950 2955 2960 2965 2970 2975 2980 2985 2990 2995 3000 3005 3010 3015 3020 3025 3030 3035 3040 3045 3050 3055 3060 3065 3070 3075 3080 3085 3090 3095 3100 3105 3110 3115 3120 3125 3130 3135 3140 3145 3150 3155 3160 3165 3170 3175 3180 3185 3190 3195 3200 3205 3210 3215 3220 3225 3230 3235 3240 3245 3250 3255 3260 3265 3270 3275 3280 3285 3290 3295 3300 3305 3310 3315 3320 3325 3330 3335 3340 3345 3350 3355 3360 3365 3370 3375 3380 3385 3390 3395 3400 3405 3410 3415 3420 3425 3430 3435 3440 3445 3450 3455 3460 3465 3470 3475 3480 3485 3490 3495 3500 3505 3510 3515 3520 3525 3530 3535 3540 3545 3550 3555 3560 3565 3570 3575 3580 3585 3590 3595 3600 3605 3610 3615 3620 3625 3630 3635 3640 3645 3650 3655 3660 3665 3670 3675 3680 3685 3690 3695 3700 3705 3710 3715 3720 3725 3730 3735 3740 3745 3750 3755 3760 3765 3770 3775 3780 3785 3790 3795 3800 3805 3810 3815 3820 3825 3830 3835 3840 3845 3850 3855 3860 3865 3870 3875 3880 3885 3890 3895 3900 3905 3910 3915 3920 3925 3930 3935 3940 3945 3950 3955 3960 3965 3970 3975 3980 3985 3990 3995 4000 4005 4010 4015 4020 4025 4030 4035 4040 4045 4050 4055 4060 4065 4070 4075 4080 4085 4090 4095 4100 4105 4110 4115 4120 4125 4130 4135 4140 4145 4150 4155 4160 4165 4170 4175 4180 4185 4190 4195 4200 4205 4210 4215 4220 4225 4230 4235 4240 4245 4250 4255 4260 4265 4270 4275 4280 4285 4290 4295 4300 4305 4310 4315 4320 4325 4330 4335 4340 4345 4350 4355 4360 4365 4370 4375 4380 4385 4390 4395 4400 4405 4410 4415 4420 4425 4430 4435 4440 4445 4450 4455 4460 4465 4470 4475 4480 4485 4490 4495 4500 4505 4510 4515 4520 4525 4530 4535 4540 4545 4550 4555 4560 4565 4570 4575 4580 4585 4590 4595 4600 4605 4610 4615 4620 4625 4630 4635 4640 4645 4650 4655 4660 4665 4670 4675 4680 4685 4690 4695 4700 4705 4710 4715 4720 4725 4730 4735 4740 4745 4750 4755 4760 4765 4770 4775 4780 4785 4790 4795 4800 4805 4810 4815 4820 4825 4830 4835 4840 4845 4850 4855 4860 4865 4870 4875 4880 4885 4890 4895 4900 4905 4910 4915 4920 4925 4930 4935 4940 4945 4950 4955 4960 4965 4970 4975 4980 4985 4990 4995 5000 5005 5010 5015 5020 5025 5030 5035 5040 5045 5050 5055 5060 5065 5070 5075 5080 5085 5090 5095 5100 5105 5110 5115 5120 5125 5130 5135 5140 5145 5150 5155 5160 5165 5170 5175 5180 5185 5190 5195 5200 5205 5210 5215 5220 5225 5230 5235 5240 5245 5250 5255 5260 5265 5270 5275 5280 5285 5290 5295 5300 5305 5310 5315 5320 5325 5330 5335 5340 5345 5350 5355 5360 5365 5370 5375 5380 5385 5390 5395 5400 5405 5410 5415 5420 5425 5430 5435 5440 5445 5450 5455 5460 5465 5470 5475 5480 5485 5490 5495 5500 5505 5510 5515 5520 5525 5530 5535 5540 5545 5550 5555 5560 5565 5570 5575 5580 5585 5590 5595 5600 5605 5610 5615 5620 5625 5630 5635 5640 5645 5650 5655 5660 5665 5670 5675 5680 5685 5690 5695 5700 5705 5710 5715 5720 5725 5730 5735 5740 5745 5750 5755 5760 5765 5770 5775 5780 5785 5790 5795 5800 5805 5810 5815 5820 5825 5830 5835 5840 5845 5850 5855 5860 5865 5870 5875 5880 5885 5890 5895 5900 5905 5910 5915 5920 5925 5930 5935 5940 5945 5950 5955 5960 5965 5970 5975 5980 5985 5990 5995 6000 6005 6010 6015 6020 6025 6030 6035 6040 6045 6050 6055 6060 6065 6070 6075 6080 6085 6090 6095 6100 6105 6110 6115 6120 6125 6130 6135 6140 6145 6150 6155 6160 6165 6170 6175 6180 6185 6190 6195 6200 6205 6210 6215 6220 6225 6230 6235 6240 6245 6250 6255 6260 6265 6270 6275 6280 6285 6290 6295 6300 6305 6310 6315 6320 6325 6330 6335 6340 6345 6350 6355 6360 6365 6370 6375 6380 6385 6390 6395 6400 6405 6410 6415 6420 6425 6430 6435 6440 6445 6450 6455 6460 6465 6470 6475 6480 6485 6490 6495 6500 6505 6510 6515 6520 6525 6530 6535 6540 6545 6550 6555 6560 6565 6570 6575 6580 6585 6590 6595 6600 6605 6610 6615 6620 6625 6630 6635 6640 6645 6650 6655 6660 6665 6670 6675 6680 6685 6690 6695 6700 6705 6710 6715 6720 6725 6730 6735 6740 6745 6750 6755 6760 6765 6770 6775 6780 6785 6790 6795 6800 6805 6810 6815 6820 6825 6830 6835 6840 6845 6850 6855 6860 6865 6870 6875 6880 6885 6890 6895 6900 6905 6910 6915 6920 6925 6930 6935 6940 6945 6950 6955 6960 6965 6970 6975 6980 6985 6990 6995 7000 7005 7010 7015 7020 7025 7030 7035 7040 7045 7050 7055 7060 7065 7070 7075 7080 7085 7090 7095 7100 7105 7110 7115 7120 7125 7130 7135 7140 7145 7150 7155 7160 7165 7170 7175 7180 7185 7190 7195 7200 7205 7210 7215 7220 7225 7230 7235 7240 7245 7250 7255 7260 7265 7270 7275 7280 7285 7290 7295 7300 7305 7310 7315 7320 7325 7330 7335 7340 7345 7350 7355 7360 7365 7370 7375 7380 7385 7390 7395 7400 7405 7410 7415 7420 7425 7430 7435 7440 7445 7450 7455 7460 7465 7470 7475 7480 7485 7490 7495 7500 7505 7510 7515 7520 7525 7530 7535 7540 7545 7550 7555 7560 7565 7570 7575 7580 7585 7590 7595 7600 7605 7610 7615 7620 7625 7630 7635 7640 7645 7650 7655 7660 7665 7670 7675 7680 7685 7690 7695 7700 7705 7710 7715 7720 7725 7730 7735 7740 7745 7750 7755 7760 7765 7770 7775 7780 7785 7790 7795 7800 7805 7810 7815 7820 7825 7830 7835 7840 7845 7850 7855 7860 7865 7870 7875 7880 7885 7890 7895 7900 7905 7910 7915 7920 7925 7930 7935 7940 7945 7950 7955 7960 7965 7970 7975 7980 7985 7990 7995 8000 8005 8010 8015 8020 8025 8030 8035 8040 8045 8050 8055 8060 8065 8070 8075 8080 8085 8090 8095 8100 8105 8110 8115 8120 8125 8130 8135 8140 8145 8150 8155 8160 8165 8170 8175 8180 8185 8190 8195 8200 8205 8210 8215 8220 8225 8230 8235 8240 8245 8250 8255 8260 8265 8270 8275 8280 8285 8290 8295 8300 8305 8310 8315 8320 8325 8330 8335 8340 8345 8350 8355 8360 8365 8370 8375 8380 8385 8390 8395 8400 8405 8410 8415 8420 8425 8430 8435 8440 8445 8450 8455 8460 8465 8470 8475 8480 8485 8490 8495 8500 8505 8510 8515 8520 8525 8530 8535 8540 8545 8550 8555 8560 8565 8570 8575 8580 8585 8590 8595 8600 8605 8610 8615 8620 8625 8630 8635 8640 8645 8650 8655 8660 8665 8670 8675 8680 8685 8690 8695 8700 8705 8710 8715 8720 8725 8730 8735 8740 8745 8750 8755 8760 8765 8770 8775 8780 8785 8790 8795 8800 8805 8810 8815 8820 8825 8830 8835 8840 8845 8850 8855 8860 8865 8870 8875 8880 8885 8890 8895 8900 8905 8910 8915 8920 8925 8930 8935 8940 8945 8950 8955 8960 8965 8970 8975 8980 8985 8990 8995 9000 9005 9010 9015 9020 9025 9030 9035 9040 9045 9050 9055 9060 9065 9070 9075 9080 9085 9090 9095 9100 9105 9110 9115 9120 9125 9130 9135 9140 9145 9150 9155 9160 9165 9170 9175 9180 9185 9190 9195 9200 9205 9210 9215 9220 9225 9230 9235 9240 9245 9250 9255 9260 9265 9270 9275 9280 9285 9290 9295 9300 9305 9310 9315 9320 9325 9330 9335 9340 9345 9350 9355 9360 9365 9370 9375 9380 9385 9390 9395 9400 9405 9410 9415 9420 9425 9430 9435 9440 9445 9450 9455 9460 9465 9470 9475 9480 9485 9490 9495 9500 9505 9510 9515 9520 9525 9530 9535 9540 9545 9550 9555 9560 9565 9570 9575 9580 9585 9590 9595 9600 9605 9610 9615 9620 9625 9630 9635 9640 9645 9650 9655 9660 9665 9670 9675 9680 9685 9690 9695 9700 9705 9710 9715 9720 9725 9730 9735 9740 9745 9750 9755 9760 9765 9770 9775 9780 9785 9790 9795 9800 9805 9810 9815 9820 9825 9830 9835 9840 9845 9850 9855 9860 9865 9870 9875 9880 9885 9890 9895 9900 9905 9910 9915 9920 9925 9930 9935 9940 9945 9950 9955 9960 9965 9970 9975 9980 9985 9990 9995 10000 10005 10010 10015 10020 10025 10030 10035 10040 10045 10050 10055 10060 10065 10070 10075 10080 10085 10090 10095 10100 10105 10110 10115 10120 10125 10130 10135 10140 10145 10150 10155 10160 10165 10170 10175 10180 10185 10190 10195 10200 10205 10210 10215 10220 10225 10230 10235 10240 10245 10250 10255 10260 10265 10270 10275 10280 10285 10290 10295 10300 10305 10310 10315 10320 10325 10330 10335 10340 10345 10350 10355 10360 10365 10370 10375 10380 10385 10390 10395 10400 10405 10410 10415 10420 10425 10430 10435 10440 10445 10450 10455 10460 10465 10470 10475 10480 10485 10490 10495 10500 10505 10510 10515 10520 10525 10530 10535 10540 10545 10550 10555 10560 10565 10570 10575 10580 10585 10590 10595 10600 10605 10610 10615 10620 10625 10630 10635 10640 10645 10650 10655 10660 10665 10670 10675 10680 10685 10690 10695 10700 10705 10710 10715 10720 10725 10730 10735 10740 10745 10750 10755 10760 10765 10770 10775 10780 10785 10790 10795 10800 10805 10810 10815 10820 10825 10830 10835 10840 10845 10850 10855 10860 10865 10870 10875 10880

Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg			
425	430	435	
gcg ttg ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga			1520
Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly			
440	445	450	
ttc att gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat			1568
Phe Ile Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp			
455	460	465	
gag cag gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag			1616
Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys			
470	475	480	
cct cat ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg			1664
Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu			
485	490	495	500
cct aac atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc ctg			1712
Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg Leu			
505	510	515	
aag cag ctt ggc cca gcc gcg ttt gct cgt gat ctc cgt gag cag gag			1760
Lys Gln Leu Gly Pro Ala Ala Phe Ala Arg Asp Leu Arg Glu Gln Asp			
520	525	530	
gca ctg gca gtt act gat acc acc ttc cgc gat gca cac cag tct ttg			1808
Ala Leu Ala Val Thr Asp Thr Phe Arg Asp Ala His Gln Ser Leu			
535	540	545	
ctt gcg acc cga gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc			1856
Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala			
550	555	560	
gtc gca aag ctg act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc			1904
Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly			
565	570	575	580
gcg acc tac gat gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac			1952
Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp			
585	590	595	
agg ctc gac gag ctg cgc gag gcg atg ccg aat gta aac att cag atg			2000
Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met			
600	605	610	
ctg ctt cgc ggc cgc aac acc gtg gga tac acc ccg tac cca gac tcc			2048

Leu	Leu	Arg	Gly	Arg	Asn	Thr	Val	Gly	Tyr	Thr	Pro	Tyr	Pro	Asp	Ser		
615							620				625						
gtc tgc cgc gcg ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc															2096		
Val	Cys	Arg	Ala	Phe	Val	Lys	Glu	Ala	Ala	Ser	Ser	Gly	Val	Asp	Ile		
630					635					640							
ttc cgc atc ttc gac gcg ctt aac gac gtc tcc cag atg cgt cca gca															2144		
Phe	Arg	Ile	Phe	Asp	Ala	Leu	Asn	Asp	Val	Ser	Gln	Met	Arg	Pro	Ala		
645					650				655			660					
atc gac gca gtc ctg gag acc aac acc gcg gta gcc gag gtg gct atg															2192		
Ile	Asp	Ala	Val	Leu	Glu	Thr	Asn	Thr	Ala	Val	Ala	Glu	Val	Ala	Met		
							665	670			675						
gct tat tct ggt gat ctc tct gat cca aat gaa aag ctc tac acc ctg															2240		
Ala	Tyr	Ser	Gly	Asp	Leu	Ser	Asp	Pro	Asn	Glu	Lys	Leu	Tyr	Thr	Leu		
					680.			685			690						
gat tac tac cta aag atg gca gag gag atc gtc aag tct ggc gct cac															2288		
Asp	Tyr	Tyr	Leu	Lys	Met	Ala	Glu	Glu	Ile	Val	Lys	Ser	Gly	Ala	His		
					695			700			705						
atc ttg gcc att aag gat atg gct ggt ctg ctt cgc cca gct gcg gta															2336		
Ile	Leu	Ala	Ile	Lys	Asp	Met	Ala	Gly	Leu	Leu	Arg	Pro	Ala	Ala	Val		
					710			715			720						
acc aag ctg gtc acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac															2384		
Thr	Lys	Leu	Val	Thr	Ala	Leu	Arg	Arg	Glu	Phe	Asp	Leu	Pro	Val	His		
					725			730			735			740			
gtg cac acc cac gac act gcg ggt ggc cag ctg gca acc tac ttt gct															2432		
Val	His	Thr	Asp	Thr	Ala	Gly	Gly	Gln	Leu	Ala	Thr	Tyr	Phe	Ala			
					745			750			755						
gca gct caa gct ggt gca gat gct gtt gac ggt gct tcc gca cca ctg															2480		
Ala	Ala	Gln	Ala	Gly	Ala	Asp	Ala	Val	Asp	Gly	Ala	Ser	Ala	Pro	Leu		
					760			765			770						
tct ggc acc acc tcc cag cca tcc ctg tct gcc att gtt gct gca ttc															2528		
Ser	Gly	Thr	Ser	Gln	Pro	Ser	Leu	Ser	Ala	Ile	Val	Ala	Ala	Phe			
					775			780			785						
gcg cac acc cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac															2576		
Ala	His	Thr	Arg	Arg	Asp	Thr	Gly	Leu	Ser	Leu	Glu	Ala	Val	Ser	Asp		
					790			795			800						
ctc gag ccg tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag															2624		

Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu			
805	810	815	820
tct gga acc cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca			2672
Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro			
825	830	835	
ggc gga cag ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt			2720
Gly Gly Gln Leu Ser Asn Leu Arg Ala Gin Ala Thr Ala Leu Gly Leu			
840	845	850	
gcg gat cgt ttc gaa ctc atc gaa gac aac tac gca gcc gtt aat gag			2768
Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ala Val Asn Glu			
855	860	865	
atg ctg gga cgc cca acc aag gtc acc cca tcc tcc aag gtt gtt ggc			2816
Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly			
870	875	880	
gac ctc gca ctc cac ctc gtt ggt gcg ggt gtg gat cca gca gac ttt			2864
Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe			
885	890	895	900
gct gcc gat cca caa aag tac gac atc cca gac tct gtc atc gcg ttc			2912
Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe			
905	910	915	
ctg cgc ggc gag ctt ggt aac cct cca ggt ggc tgg cca gag cca ctg			2960
Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu			
920	925	930	
cgc acc cgc gca ctg gaa ggc cgc tcc gaa ggc aag gca cct ctg acg			3008
Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr			
935	940	945	
gaa gtt cct gag gaa gag cag gcg cac ctc gac gct gat gat tcc aag			3056
Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys			
950	955	960	
gaa cgt cgc aat agc ctc aac cgc ctg ctg ttc ccg aag cca acc gaa			3104
Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu			
965	970	975	980
gag ttc ctc gag cac cgt cgc ttc ggc aac acc tct gcg ctg gat			3152
Glu Phe Leu Glu His Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp			
985	990	995	
gat cgt gaa ttc ttc tac ggc ctg gtc gaa ggc cgc gag act ttg atc			3200

Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
 1000 1005 1010
 3248
 cgc ctg cca gat gtg cgc acc cca ctg ctt gtt cgc ctg gat gcg atc
 Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
 1015 1020 1025
 tct gag cca gac gat aag ggt atg cgc aat gtt gtg gcc aac gtc aac
 Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
 1030 1035 1040
 3296
 ggc cag atc cgc cca atg cgt gtg cgt gac cgc tcc gtt gag tct gtc
 Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
 1045 1050 1055 1060
 acc gca acc gca gaa aag gca gat tcc tcc aac aag ggc cat gtt gct
 Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
 1065 1070 1075
 3344
 gca cca ttc gct ggt gtt gtc acc gtg act gtt gct gaa ggt gat gag
 Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
 1080 1085 1090
 gtc aag gct gga gat gca gtc gca atc atc gag gct atg aag atg gaa
 Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
 1095 1100 1105
 3440
 gca aca atc act gct tct gtt gac ggc aaa atc gat cgc gtt gtg gtt
 Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val
 1110 1115 1120
 3488
 cct gct gca acg aag gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc
 Pro Ala Ala Thr Lys Val Glu Gly Asp Leu Ile Val Val Val Ser
 1125 1130 1135 1140
 3536
 taa acctttctgt aaaaagcccc gcgttccct catggaggag gcggggcttt
 3584
 ttggggccaag atggagatg ggtgagttgg atttggcttg attcgacact tttaaggc
 gagatttgaa gatggagacc aaggctcaaa g
 3637
 3697
 3728

<210> 2
 <211> 1140
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2

Val Ser Thr His Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu
1 5 10 15
Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu
20 25 30
Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly
35 40 45
Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu
50 55 60
Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala
65 70 75 80
Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu
85 90 95
Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr
100 105 110
Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser
115 120 125
Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu
130 135 140
Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly
145 150 155 160
Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Arg
165 170 175
Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr
180 185 190
Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr
195 200 205
Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile Leu
210 215 220
Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser
225 230 235 240
Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His
245 250 255
Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe
260 265 270
Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val
275 280 285
Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln
290 295 300
Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val Lys
305 310 315 320
Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu
325 330 335
Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg Ile
340 345 350
Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile
355 360 365
Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala

370	375	380
Ala Gln Leu Gly Gly	Glu Ile Thr Ala His Phe Asp Ser Met	Leu Val
385	390	395
Lys Met Thr Cys Arg	Gly Ser Asp Phe Glu Thr Ala Val Ala Arg Ala	
405	410	415
Gln Arg Ala Leu Ala	Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile	
420	425	430
Gly Phe Leu Arg Ala	Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg	
435	440	445
Ile Ala Thr Gly Phe	Ile Ala Asp His Pro His Leu Leu Gln Ala Pro	
450	455	460
Pro Ala Asp Asp Glu	Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val	
465	470	475
Thr Val Asn Lys Pro	His Gly Val Arg Pro Lys Asp Val Ala Ala Pro	
485	490	495
Ile Asp Lys Leu Pro	Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser	
500	505	510
Arg Asp Arg Leu Lys	Gln Leu Gly Pro Ala Ala Phe Ala Arg Asp Leu	
515	520	525
Arg Glu Gln Asp Ala	Leu Ala Val Thr Asp Thr Phe Arg Asp Ala	
530	535	540
His Gln Ser Leu Leu	Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro	
545	550	555
Ala Ala Glu Ala Val	Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu	
565	570	575
Ala Trp Gly Ala Thr	Tyr Asp Val Ala Met Arg Phe Leu Phe Glu	
580	585	590
Asp Pro Trp Asp Arg	Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val	
595	600	605
Asn Ile Gln Met Leu	Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro	
610	615	620
Tyr Pro Asp Ser Val	Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser	
625	630	635
Gly Val Asp Ile Phe	Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln	
645	650	655
Met Arg Pro Ala Ile	Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala	
660	665	670
Glu Val Ala Met Ala	Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys	
675	680	685
Leu Tyr Thr Leu Asp	Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys	
690	695	700
Ser Gly Ala His Ile	Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg	
705	710	715
Pro Ala Ala Val Thr	Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp	
725	730	735
Leu Pro Val His Val	His Thr His Asp Thr Ala Gly Gly Gln Leu Ala	
740	745	750
Thr Tyr Phe Ala Ala	Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala	

755	760	765
Ser Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala Ile		
770	775	780
Val Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu		
785	790	795
Ala Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr		
805	810	815
Leu Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg		
820	825	830
His Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr		
835	840	845
Ala Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala		
850	855	860
Ala Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser		
865	870	875
Lys Val Val Gly Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp		
885	890	895
Pro Ala Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser		
900	905	910
Val Ile Ala Phe Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp		
915	920	925
Pro Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys		
930	935	940
Ala Pro Leu Thr Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala		
945	950	955
Asp Asp Ser Lys Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro		
965	970	975
Lys Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr		
980	985	990
Ser Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg		
995	1000	1005
Glu Thr Leu Ile Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg		
1010	1015	1020
Leu Asp Ala Ile Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val		
1025	1030	1035
Ala Asn Val Asn Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser		
1045	1050	1055
Val Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys		
1060	1065	1070
Gly His Val Ala Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala		
1075	1080	1085
Glu Gly Asp Glu Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala		
1090	1095	1100
Met Lys Met Glu Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp		
1105	1110	1115
Arg Val Val Val Pro Ala Ala Thr Lys Val Glu Gly Asp Leu Ile		
1125	1130	1135
Val Val Val Ser		

1140

<210> 3
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 3
cgtcttcatc gaaatgaac

19

<210> 4
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 4
acggtggtga tccggcact

19